



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hinuma, Shuji
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko

(ii) TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE

(iii) NUMBER OF SEQUENCES: 140

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/776,971
(B) FILING DATE: 07-FEB-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/JP96/03821
(B) FILING DATE: 28-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 7/343371
(B) FILING DATE: 28-DEC-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 8/59419
(B) FILING DATE: 15-MAR-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 8/211805
(B) FILING DATE: 12-AUG-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 8/246573
(B) FILING DATE: 18-SEP-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 27,026
(C) REFERENCE/DOCKET NUMBER: 47176

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Lys	Ala	Val	Gly	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Gly	Leu
1				5				10					15	
Ala	Leu	Gln	Gly	Ala	Ala	Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu Ile
		20					25					30		
Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile Arg
	35					40					45			
Pro	Val	Gly	Arg	Phe	Gly	Arg	Arg	Ala	Ala	Pro	Gly	Asp	Gly	Pro
	50				55					60				
Arg	Pro	Gly	Pro	Arg	Arg	Val	Pro	Ala	Cys	Phe	Arg	Leu	Glu	Gly Gly
65				70				75					80	
Ala	Glu	Pro	Ser	Arg	Ala	Leu	Pro	Gly	Arg	Leu	Thr	Ala	Gln	Leu Val
				85				90					95	
Gln	Glu													

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAAGGCGG	TGGGGGCGCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG	60
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	CCCCCGACAT	CAACCCTGCC	120
TGGTACGCRG	GCCGTGGGAT	CCGGCCCCGTG	GGCCGCTTCG	GCCGGCGAAG	AGCTGCCCCY	180
GGGGACGGAC	CCAGGCCTGG	CCCCCGGCGT	GTGCCGGCCT	GCTTCCGCCT	GGAAGGCGGY	240
GCTGAGCCCT	CCCGAGCCCT	CCCGGGGCGG	CTGACGGCCC	AGCTGGTCCA	GGAA	294

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1			5						10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly			
		20					25								

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg													

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	
		20					25					30			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

Arg

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe
 20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe Gly
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe Gly Arg
 20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC 60
GCRGGCCCGTG GGATCCGGCC CGTGGGC 87

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGC 57

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC 60
GCRGGCCCGTG GGATCCGGCC CGTGGGCCGC TTC 93

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC 60
GCRGGCCCGTG GGATCCGGCC CGTGGGCCGC TTCGGC 96

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC	60
GCRGGCCCGTG GGATCCGGCC CGTGGGCCGC TTCGGCCGG	99

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCCGT GGGCCGCTTC	60
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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCCGT GGGCCGCTTC	60
GGC	63

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCCGT GGGCCGCTTC	60
GGCCGG	66

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn
1				5				10						15	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
			20					25					30		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
		35					40					45			
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	50					55					60				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
65					70					75					80
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile					
				85						90					

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu
1				5				10					15		
Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly
			20					25					30		
Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg
		35					40					45			
Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val					
	50						55								

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met 1	Ala	Ser	Ser	Thr 5	Thr	Arg	Gly	Pro	Arg 10	Val	Ser	Asp	Leu 15	Phe	Ser
Gly	Leu	Pro	Pro	Ala	Val	Thr	Thr	Pro	Ala	Asn	Gln	Ser	Ala	Glu	Ala
			20					25					30		
Ser	Ala	Gly	Asn	Gly	Ser	Val	Ala	Gly	Ala	Asp	Ala	Pro	Ala	Val	Thr
		35					40					45			
Pro	Phe	Gln	Ser	Leu	Gln	Leu	Val	His	Gln	Leu	Lys	Gly	Leu	Ile	Val
	50					55					60				
Leu	Leu	Tyr	Ser	Val	Val	Val	Val	Val	Gly	Leu	Val	Gly	Asn	Cys	Leu
65				70						75				80	
Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn
				85					90					95	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
			100					105					110		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
		115					120					125			
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	130					135					140				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
145				150						155				160	
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser
				165					170					175	
Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu
			180					185					190		
Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val
		195					200					205			
Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu
	210					215					220				
Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val
225				230						235				240	
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
				245					250					255	
Val	Pro	Gly	Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
			260					265					270		
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Ala
		275					280					285			
Val	Cys	Trp	Leu	Pro	Leu	His	Val	Phe	Asn	Leu	Leu	Arg	Asp	Leu	Asp
	290					295					300				
Pro	His	Ala	Ile	Asp	Pro	Tyr	Ala	Phe	Gly	Leu	Val	Gln	Leu	Leu	Cys
305				310						315				320	
His	Trp	Leu	Ala	Met	Ser	Ser	Ala	Cys	Tyr	Asn	Pro	Phe	Ile	Tyr	Ala
				325					330					335	
Trp	Leu	His	Asp	Ser	Phe	Arg	Glu	Glu	Leu	Arg	Lys	Leu	Leu	Val	Ala
			340					345					350		
Trp	Pro	Arg	Lys	Ile	Ala	Pro	His	Gly	Gln	Asn	Met				

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu Tyr Asn Val Thr Asn
1           5           10           15
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
20           25           30
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
35           40           45
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr
50           55           60
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65           70           75           80
Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
85           90           95
Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu
100          105          110
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
115          120          125
Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
130          135          140
Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
145          150          155          160
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
165          170          175
Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
180          185          190
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
195          200          205

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser
1				5					10					15	
Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu
			20					25					30		
Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val
			35				40						45		
Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Ile
	50					55					60				
Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala
65					70				75					80	
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
				85					90					95	
Val	Pro	Gly	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
			100					105					110		
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Val	
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGGTGCTGG	TGATCGCGCG	GGTGCGCCCG	CTGCACAACG	TGACGAACTT	CCTCATCGGC	60
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	120
GCCTTCGAGC	CACGCGGCTG	GGTGTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	180
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTT	ACGCTCACCA	CCATCGCAGT	GGACCGGTAC	240
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATC			273

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGCCTGCTGC	TGGTCACCTA	CCTGCTCCCT	CTGCTGGTCA	TCCTCCTGTC	TTACGTCCGG	60
GTGTCAGTGA	AGCTCCGCAA	CCGCGTGGTG	CCGGGCTGCG	TGACCCAGAG	CCAGGCCGAC	120
TGGGACCGCG	CTCGGCGCCG	GCGCACCTTC	TGCTTGCTGG	TGGTGGTCGT	GGTGGTG	177

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGCCTCAT	CGACCACTCG	GGGCCCCAGG	GTTTCTGACT	TATTTTCTGG	GCTGCCGCCG	60
GCGGTCACAA	CTCCCGCCAA	CCAGAGCGCA	GAGGCCTCGG	CGGGCAACGG	GTCGGTGGCT	120
GGCGCGGACG	CTCCAGCCGT	CACGCCCTTC	CAGAGCCTGC	AGCTGGTGCA	TCAGCTGAAG	180
GGGCTGATCG	TGCTGCTCTA	CAGCGTCGTG	GTGGTCGTGG	GGCTGGTGGG	CAACTGCCTG	240
CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGCACAACG	TGACGAACTT	CCTCATCGGC	300
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	360
GCCTTCGAGC	CACGCGGCTG	GGTGTTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	420
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTT	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	480
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	540
CTGGCCATCT	GGGCGCTGTC	CGCGGTGCTG	GCGCTGCCCG	CCGCCGTGCA	CACCTATCAC	600
GTGGAGCTCA	AGCCGCACGA	CGTGCGCCTC	TGCGAGGAGT	TCTGGGGCTC	CCAGGAGCGC	660
CAGCGCCAGC	TCTACGCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	720
ATCCTCCTGT	CTTACGTCCG	GGTGTCAGTG	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCTGC	780
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGCGCC	GGCGCACCTT	CTGCTTGCTG	840
GTGGTGGTCTG	TGGTGGTGTT	CGCCGTCTGC	TGGCTGCCGC	TGCACGTCTT	CAACCTGCTG	900
CGGGACCTCG	ACCCCCACGC	CATCGACCTT	TACGCCTTTG	GGCTGGTGCA	GCTGCTCTGC	960
CACTGGCTCG	CCATGAGTTC	GGCCTGCTAC	AACCCCTTCA	TCTACGCCTG	GCTGCACGAC	1020
AGCTTCCGCG	AGGAGCTGCG	CAAACGTGTT	GTCGCTTGGC	CCCGAAGAT	AGCCCCCAT	1080
GGCCAGAATA	TGACCGTCAG	CGTGGTCATC				1110

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 618 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGTACAACG	TGACGAATTT	CCTCATCGGC	60
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	120
GCCTTCGAGC	CACGCGGCTG	GGTGTTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	180
CAGGCGGTCA	CCGTCTATGT	GTCGGTGTTT	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	240
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	300
CTGGCCATCT	GGGTGCTGTC	CGCGGTGCTG	GCGCTGCCCG	CCGCCGTGCA	CACCTATCAC	360
GTGGAGCTCA	AGCCGCACGA	CGTGCGCCTC	TGCGAGGAGT	TCTGGGGCTC	CCAGGAGCGC	420
CAGCGCCAGC	TCTACGCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	480
ATCCTCCTGT	CTTACGCCCC	GGTGTCAGTG	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCCGC	540
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGCGCC	GGCGCACCTT	CTGCTTGCTG	600
GTGGTGGTCTG	TGGTGGTG					618

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGGTTCTGG TGCACCCGCT ACCTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG	60
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT	120
GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCAGGAGT TCTGGGGCTC GCAGGAGCGC	180
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC	240
ATCCTCCTGT CTTACGTACG GGTGTCACTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC	300
GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG	360
GTGGTGGTGG TGGTAGTG	378

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGTGGSCMTS STGGGCAACN YCCTG	25
-----------------------------	----

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTNGWRRGGC ANCCAGCAGA KGGCAAA	27
-------------------------------	----

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGTGYGYSA TYGCNNTKGA YMGSTAC

27

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA

29

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGACTTATT TTCTGGGCTG CCGC

24

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

- (2) INFORMATION FOR SEQ ID NO:35:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
 - (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /mod_base= i
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

- (2) INFORMATION FOR SEQ ID NO:36:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
 - (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /mod_base= i
 - (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /mod_base= i
 - (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 18
 - (D) OTHER INFORMATION: /mod_base= i
 - (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 24
 - (D) OTHER INFORMATION: /mod_base= i
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 15
 - (D) OTHER INFORMATION: /mod_base= i
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 21
 - (D) OTHER INFORMATION: /mod_base= i
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACGGGCCCKDA TGCCNCKGCC NGCRTA

26

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCGGCGTACC AGGCAGGGTT

20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGGCAGGGTT GATGTCGGGG GTGCGGAT

28

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCAGCAG AGCCCACCAG CACTCCA

27

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGGGGGCCT GGCTCCTCTG CCTGCTG

27

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTGTGACGA ATGAAGGCGG TGGGGGCCTG GC

32

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid

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(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "synthetic DNA"
```

AGGCTCCCGC TGTTATTCCT GGAC

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Met Ala Leu Lys Thr Trp Leu Leu Cys Leu Leu Leu Leu Ser Leu Val
1 5 10 15
Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg

[illegible]

(2) INFORMATION FOR SEO ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGGCCCTGA	AGACGTGGCT	TCTGTGCTTG	CTGCTGCTAA	GCTTGGTCCT	CCCAGGGGCT	60
TCCAGCCGAG	CCCACCAGCA	CTCCATGGAG	ACAAGAACCC	CTGATATCAA	TCCTGCCTGG	120
TACACGGGCC	GCGGGATCAG	GCCTGTGGGC	CGCTTCGGCA	GGAGAAGGGC	AACCCCGAGG	180
GATGTCAC TG	GACTTGGCCA	ACTCAGCTGC	CTCCCACTGG	ATGGACGCAC	CAAGTTCTCT	240
CAGCGTGA						249

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Thr	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Thr	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

Arg

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg	Phe												
			20												

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg	Phe	Gly											
				20											

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg	Phe	Gly	Arg										
				20											

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGCCGAGCCC	ACCAGCACTC	CATGGAGACA	AGAACCCTG	ATATCAATCC	TGCCTGGTAC	60
ACGGGCCGCG	GGATCAGGCC	TGTGGGCCGC	TTC			93

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC	60
ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGGC	96

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC	60
ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGGCAGG	99

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC	60
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(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC	60
GGC	63

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGCAGG 66

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Lys Val Leu Arg Ala Trp Leu Leu Cys Leu Leu Met Leu Gly Leu
1 5 10 15
Ala Leu Arg Gly Ala Ala Ser Arg Thr His Arg His Ser Met Glu Ile
20 25 30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg
35 40 45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Leu Gly Asp Val Pro
50 55 60
Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys Phe Pro Leu Glu Gly Gly
65 70 75 80
Ala Met Ser Ser Gln Asp Gly
85

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGAAGGTGC	TGAGGGCCTG	GCTCCTGTGC	CTGCTGATGC	TGGGCCTGGC	CCTGCGGGGA	60
GCTGCAAGTC	GTACCCATCG	GCACTCCATG	GAGATCCGCA	CCCCTGACAT	CAATCCTGCC	120
TGGTACGCCA	GTCGCGGGAT	CAGGCCTGTG	GGCCGCTTCG	GTCGGAGGAG	GGCAACCCTG	180
GGGGACGTCC	CCAAGCCTGG	CCTGCGACCC	CGGCTGACCT	GCTTCCCCCT	GGAAGGCGGT	240
GCTATGTCGT	CCCAGGATGG	C				261

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10					15		
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	
		20					25					30			

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10					15		
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
		20					25					30			

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10					15		
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20				25					30			
Arg															

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro
1			5					10					15		
Val	Gly	Arg	Phe												
			20												

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro
1			5					10					15		
Val	Gly	Arg	Phe	Gly											
			20												

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro
1			5					10					15		
Val	Gly	Arg	Phe	Gly	Arg										
			20												

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AGTCGTACCC	ATCGGCACTC	CATGGAGATC	CGCACCCCTG	ACATCAATCC	TGCCTGGTAC	60
GCCAGTCGCG	GGATCAGGCC	TGTGGGCCGC	TTC			93

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGTCGTACCC	ATCGGCACTC	CATGGAGATC	CGCACCCCTG	ACATCAATCC	TGCCTGGTAC	60
GCCAGTCGCG	GGATCAGGCC	TGTGGGCCGC	TTCGGT			96

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGTCGG 99

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGT 63

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGTCGG 66

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "Ala or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "Gly or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21..22
- (D) OTHER INFORMATION: /product= "may be a Gly-Arg or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Xaa	Xaa	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg	Phe	Xaa	Xaa										
			20												

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "Ala or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "Ile or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser	Arg	Xaa	His	Xaa	His	Ser	Met	Glu	Xaa	Arg
1				5					10	

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CARCAYTCCA TGGAGACAAG AACCCC

26

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TACCAGGCAG GATTGATACA GGGG

24

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCATCATCC AGGAAGACGG AGCAT

25

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AGCAGAGGAG AGGGAGGGTA GAGGA

25

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACGTGGCTTC TGTGCTTGCT GC

22

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCCTGATCCC GCGGCCCGTG TACCA

25

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTGCCCTTCT CCTGCCGAAG CGGCCC

26

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGCGGGGGCT GCAAGTCGTA CCCATCG

27

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CGGCACTCCA TGGAGATCCG CACCCCT

27

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGCAGGAT TGATGTCAGG GGTGCGG

27

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CATGGAGTGC CGATGGGTAC GACTTGC

27

- (2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGCCTCCTCG GAGGAGCCAA GGGATGA

27

- (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGGAAAGGAG CCCGAAGGAG AGGAGAG

27

- (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CCTGCTGGCC ATTCTCCTGT CTTAC

25

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGGTCCAGGT CCCGCAGAAG GTTGA

25

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAAGACGGAG CATGGCCCTG AAGAC

25

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGCTGAG TTGGCCAAGT CCACT

25

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Cys	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Cys	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTACACAGGT CGACATGACC TCAC

24

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTCAGAGCTA GCAGAGTGTC ATCAG

25

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10					15		
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	
		20					25						30		

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro
1			5					10					15		
Val	Gly	Arg	Phe												
		20													

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...669
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTG GGC ATG GTG GGC AAC ATC CTG CTG GTG CTG GTG ATC GCG CGG GTG	48
Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val	
1 5 10 15	
CGC CGG CTG TAC AAC GTG ACG AAT TTC CTC ATC GGC AAC CTG GCC TTG	96
Arg Arg Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu	
20 25 30	
TCC GAC GTG CTC ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT	144
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr	
35 40 45	
GCC TTC GAG CCA CGC GGC TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG	192
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu	
50 55 60	
GTC TTC TTC CTG CAG GCG GTC ACC GTC TAT GTG TCG GTG TTC ACG CTC	240
Val Phe Phe Leu Gln Ala Val Thr Val Tyr Val Ser Val Phe Thr Leu	
65 70 75 80	
ACC ACC ATC GCA GTG GAC CGC TAC GTC GTG CTG GTG CAC CCG CTG AGG	288
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg	
85 90 95	
CGG CGC ATC TCG CTG CGC CTC AGC GCC TAC GCT GTG CTG GCC ATC TGG	336
Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Ala Ile Trp	
100 105 110	
GTG CTG TCC GCG GTG CTG GCG CTG CCC GCC GCC GTG CAC ACC TAT CAC	384
Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His	
115 120 125	
GTG GAG CTC AAG CCG CAC GAC GTG CGC CTC TGC GAG GAG TTC TGG GGC	432
Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly	
130 135 140	
TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG CTG GTC	480
Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Leu Val	
145 150 155 160	
ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC GCC CGG GTG	528
Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val	
165 170 175	

TCA GTG AAG CTC CGC AAC CGC GTG GTG CCG GGC CGC GTG ACC CAG AGC	576
Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser	
180 185 190	
CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG	624
Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu	
195 200 205	
GTG GTG GTC GTG GTG GTG TTC ACC CTC TGC TGG CTG CCC TTC TTC	669
Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Phe	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val	
1 5 10 15	
Arg Arg Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu	
20 25 30	
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr	
35 40 45	
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu	
50 55 60	
Val Phe Phe Leu Gln Ala Val Thr Val Tyr Val Ser Val Phe Thr Leu	
65 70 75 80	
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg	
85 90 95	
Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Ala Ile Trp	
100 105 110	
Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His	
115 120 125	
Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly	
130 135 140	
Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Leu Val	
145 150 155 160	
Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val	
165 170 175	
Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser	
180 185 190	
Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu	
195 200 205	
Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Phe	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Val	Gly	Met	Val	Gly	Asn	Val	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val
1				5					10					15	
Arg	Arg	Leu	His	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu
			20					25					30		
Ser	Asp	Val	Leu	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr
		35					40					45			
Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu
	50					55					60				
Val	Phe	Phe	Leu	Gln	Pro	Val	Thr	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu
65				70					75					80	
Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg
				85					90					95	
Arg	Arg	Ile	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val
			100					105					110		
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
	115					120						125			
Val	Pro	Gly	Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
	130					135					140				
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Ala
145					150				155						160
Ile	Cys	Trp	Leu	Pro	Tyr	Tyr									
					165										

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val	Gly	Met	Val	Gly	Asn	Ile	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val
1				5					10					15	
Arg	Arg	Leu	Tyr	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu
			20					25					30		
Ser	Asp	Val	Leu	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr
		35					40					45			
Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu
	50					55					60				
Val	Phe	Phe	Leu	Gln	Ala	Val	Thr	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu
65				70					75					80	
Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg
				85					90					95	
Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp

GTG CTG GTG ATC GCG CGG GTG CGC CGG CTG CAC AAC GTG ACG AAC TTC	408
Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn Phe	
85 90 95	
CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC ATG TGC ACC GCC TGC	456
Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala Cys	
100 105 110	
GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC TGG GTG TTC	504
Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val Phe	
115 120 125	
GGC GGC GGC CTG TGC CAC CTG GTC TTC TTC CTG CAG CCG GTC ACC GTC	552
Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr Val	
130 135 140 145	
TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGC TAC GTC	600
Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val	
150 155 160	
GTG CTG GTG CAC CCG CTG AGG CGG CGC ATC TCG CTG CGC CTC AGC GCC	648
Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala	
165 170 175	
TAC GCT GTG CTG GCC ATC TGG GCG CTG TCC GCG GTG CTG GCG CTG CCC	696
Tyr Ala Val Leu Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro	
180 185 190	
GCC GCC GTG CAC ACC TAT CAC GTG GAG CTC AAG CCG CAC GAC GTG CGC	744
Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val Arg	
195 200 205	
CTC TGC GAG GAG TTC TGG GGC TCC CAG GAG CGC CAG CGC CAG CTC TAC	792
Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu Tyr	
210 215 220 225	
GCC TGG GGG CTG CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG GTC ATC	840
Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile	
230 235 240	
CTC CTG TCT TAC GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG GTG	888
Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val	
245 250 255	
CCG GGC TGC GTG ACC CAG AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC	936
Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg	
260 265 270	
CGG CGC ACC TTC TGC TTG CTG GTG GTG GTC GTG GTG GTG TTC GCC GTC	984
Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala Val	
275 280 285	
TGC TGG CTG CCG CTG CAC GTC TTC AAC CTG CTG CGG GAC CTC GAC CCC	1032
Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp Pro	
290 295 300 305	

CAC GCC ATC GAC CCT TAC GCC TTT GGG CTG GTG CAG CTG CTC TGC CAC	1080
His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His	
310 315 320	
TGG CTC GCC ATG AGT TCG GCC TGC TAC AAC CCC TTC ATC TAC GCC TGG	1128
Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Trp	
325 330 335	
CTG CAC GAC AGC TTC CGC GAG GAG CTG CGC AAA CTG TTG GTC GCT TGG	1176
Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala Trp	
340 345 350	
CCC CGC AAG ATA GCC CCC CAT GGC CAG AAT ATG ACC GTC AGC GTG GTC	1224
Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val Val	
355 360 365	
ATC TGATGCCACT TAGCCAGGCC TTGGTCAAGG AGCTCCACTT CAACTGGCCT CCTAGG	1283
Ile	
370	
GCACCACTCG AGGTCAATCT GGTGCTTATT CTCAGCACCA GAGCTAGC	1331

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Ala	Ser	Ser	Thr	Thr	Arg	Gly	Pro	Arg	Val	Ser	Asp	Leu	Phe	Ser
1				5				10						15	
Gly	Leu	Pro	Pro	Ala	Val	Thr	Thr	Pro	Ala	Asn	Gln	Ser	Ala	Glu	Ala
			20					25					30		
Ser	Ala	Gly	Asn	Gly	Ser	Val	Ala	Gly	Ala	Asp	Ala	Pro	Ala	Val	Thr
		35					40				45				
Pro	Phe	Gln	Ser	Leu	Gln	Leu	Val	His	Gln	Leu	Lys	Gly	Leu	Ile	Val
	50				55					60					
Leu	Leu	Tyr	Ser	Val	Val	Val	Val	Gly	Leu	Val	Gly	Asn	Cys	Leu	
65				70					75					80	
Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn
				85				90						95	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
			100					105					110		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
		115					120					125			
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	130					135					140				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
145					150					155				160	
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser

CAT GTG GAG CTC AAG CCC CAC GAC GTG AGC CTC TGC GAG GAG TTC TGG	192
His Val Glu Leu Lys Pro His Asp Val Ser Leu Cys Glu Glu Phe Trp	
50 55 60	
GGC TCG CAG GAG CGC CAA CGC CAG ATC TAC GCC TGG GGG CTG CTT CTG	240
Gly Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu	
65 70 75 80	
GGC ACC TAT TTG CTC CCC CTG CTG GCC ATC CTC CTG TCT TAC GTA CGG	288
Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg	
85 90 95	
GTG TCA GTG AAG CTG AGG AAC CGC GTG GTG CCT GGC AGC GTG ACC CAG	336
Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln	
100 105 110	
AGT CAA GCT GAC TGG GAC CGA GCG CGT CGC CGC CGC ACT TTC TGT CTG	384
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu	
115 120 125	
CTG GTG GTG GTG GTG GTA GTG TTC ACG CTC TGC TGG CTG CCC TTC TAC C	433
Leu Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr	
130 135 140	
T	434

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu	
1 5 10 15	
Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile	
20 25 30	
Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr	
35 40 45	
His Val Glu Leu Lys Pro His Asp Val Ser Leu Cys Glu Glu Phe Trp	
50 55 60	
Gly Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu	
65 70 75 80	
Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg	
85 90 95	
Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln	
100 105 110	
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu	
115 120 125	
Leu Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr	

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val
 1           5           10           15
Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu
      20           25           30
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr
      35           40           45
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu
      50           55           60
Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu
      65           70           75           80
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg
      85           90           95
Arg Arg Ile Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
      100          105          110
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
      115          120          125
Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
      130          135          140
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala
      145          150          155          160
Ile Cys Trp Leu Pro Tyr Tyr
      165

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val
 1           5           10           15
Arg Arg Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu
      20           25           30
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr
      35           40           45
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu
      50           55           60
Val Phe Phe Leu Gln Ala Val Thr Val Tyr Val Ser Val Phe Thr Leu
      65           70           75           80

```

Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg
				85					90					95	
Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp
			100					105					110		
Val	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His
		115					120					125			
Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly
	130					135					140				
Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val
145					150					155					160
Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Ala	Arg	Val
				165					170					175	
Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	Arg	Val	Thr	Gln	Ser
		180					185						190		
Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	
	195						200				205				
Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Phe	
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu
1				5					10					15	
Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile
			20					25					30		
Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr
	35					40					45				
His	Val	Glu	Leu	Lys	Pro	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp
	50					55					60				
Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu
65					70				75						80
Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile	Leu	Leu	Ser	Tyr	Val	Arg
			85					90					95		
Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	Ser	Val	Thr	Gln
		100					105					110			
Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu
	115					120					125				
Leu	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...75
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GCC	CAC	CAG	CAC	TCC	ATG	GAG	ATC	CGC	ACC	CCC	GAC	ATC	AAC	CCT	GCC	48
Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	
1				5				10						15		
TGG	TAC	GCG	GGC	CGT	GGG	ATC	CGG	CCC	G							76
Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro								
			20				25									

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala
1 5 10 15
Trp Tyr Ala Gly Arg Gly Ile Arg Pro
20 25

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 6...125
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GTGGA	ATG	AAG	GCG	GTG	GGG	GCC	TGG	CTC	CTC	TGC	CTG	CTG	CTG	CTG	GGC	50
	Met	Lys	Ala	Val	Gly	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Leu	Gly	
	1				5					10					15	

CTG GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG 98
 Leu Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu
 20 25 30

ATC CGC ACC CCC GAC ATC AAC CCT GCC T 126
 Ile Arg Thr Pro Asp Ile Asn Pro Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu
 1 5 10 15
 Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile
 20 25 30
 Arg Thr Pro Asp Ile Asn Pro Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 6...299

(D) OTHER INFORMATION:

(A) NAME/KEY: Modified Base

(B) LOCATION: 43...43

(D) OTHER INFORMATION: Xaa is Ala

(A) NAME/KEY: Modified Base

(B) LOCATION: 80...80

(D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GTGGA ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC 50
 Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly
 1 5 10 15

CTG GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG	98
Leu Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu	
20 25 30	
ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC GCR GGC CGT GGG ATC	146
Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Gly Arg Gly Ile	
35 40 45	
CGG CCC GTG GGC CGC TTC GGC CGG CGA AGA GCT GCC CCG GGG GAC GGA	194
Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly	
50 55 60	
CCC AGG CCT GGC CCC CGG CGT GTG CCG GCC TGC TTC CGC CTG GAA GGC	242
Pro Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly	
65 70 75	
GGY GCT GAG CCC TCC CGA GCC CTC CCG GGG CGG CTG ACG GCC CAG CTG	290
Xaa Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu	
80 85 90 95	
GTC CAG GAA TAACAGCGGG AGCCTGCCCC CCACCCCTCC TCCTCCACCA GCCACCTTC	348
Val Gln Glu	
CCTCCAGTCC TAATAAAAGC AGCTGGCTTG TT	380

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 43...43
- (D) OTHER INFORMATION: Xaa is Ala

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 80...80
- (D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu	
1 5 10 15	
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile	
20 25 30	
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Gly Arg Gly Ile Arg	
35 40 45	
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly Pro	
50 55 60	

Arg	Pro	Gly	Pro	Arg	Arg	Val	Pro	Ala	Cys	Phe	Arg	Leu	Glu	Gly	Xaa
65					70					75					80
Ala	Glu	Pro	Ser	Arg	Ala	Leu	Pro	Gly	Arg	Leu	Thr	Ala	Gln	Leu	Val
				85					90					95	
Gln	Glu														

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 6...299
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 43...43
- (D) OTHER INFORMATION: Xaa is Ala

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 80...80
- (D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GTGGA ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC	50
Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly	
1 5 10 15	
CTG GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG	98
Leu Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu	
20 25 30	
ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC GCR GGC CGT GGG ATC	146
Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Gly Arg Gly Ile	
35 40 45	
CGG CCC GTG GGC CGC TTC GGC CGG CGA AGA GCT GCC CTG GGG GAC GGA	194
Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly	
50 55 60	
CCC AGG CCT GGC CCC CGG CGT GTG CCG GCC TGC TTC CGC CTG GAA GGC	242
Pro Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly	
65 70 75	
GGY GCT GAG CCC TCC CGA GCC CTC CCG GGG CGG CTG ACG GCC CAG CTG	290
Xaa Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu	
80 85 90 95	
GTC CAG GAA TAACAGCGGG AGCCTGCCCC CCACCCCTCC TCCTCCACCA GCCACCTTC	348
Val Gln Glu	

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 43...43
- (D) OTHER INFORMATION: Xaa is Ala

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 80...80
- (D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu
 1           5           10           15
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile
 20           25           30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Gly Arg Gly Ile Arg
 35           40           45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly Pro
 50           55           60
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Xaa
 65           70           75           80
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
 85           90           95
Gln Glu

```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

ATGAAGGCGG TGGGGGCCTG GCTCCTCTGC CTGCTGCTGC TGGGCCTGGC CCTGCAGGGG      60
GCTGCCAGCA GAGCCCACCA GCACTCCATG GAGATCCGCA GTGAGTGTCT AGCCCCGCCC      120
CTGCCCCCAG GGGTCACAGG GGGGGCCTGG CCACTTCCTG GGCTGGGACA TCCTTGCTAA      180
GCATCCTGGG GTTGGGGTTT GGCCTCCTGT TCCCCAGACC CTTCCCCCAG GTGGCCCCGGA      240
CAGGTGCTCC CAAGGGTCCC GGCCCAGCAC ACGGGGGAGG GTCACTCCTC ACCACACGGG      300
TGGCCTGGGG CTGAGTGCAC GTCACCCATG AGAACGGGGC TGTGAGGACA GGAAAGGAAG      360

```

GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA	420
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	480
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	540
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCGAC	ATCAACCCTG	CCTGGTACGC	600
AGGCCGTGGG	ATCCGGCCCC	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG	660
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC	720
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA		769

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG	60
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC	120
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA	180
GCATCCTGGG	GTTGGGGTTT	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGGA	240
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG	300
TGGCCTGGGG	CTGAGTGAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG	360
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA	420
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	480
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	540
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCGAC	ATCAACCCTG	CCTGGTACGC	600
AGGCCGTGGG	ATCCGGCCCC	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG	660
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC	720
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA		769

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG	60
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	CCCCCGACAT	CAACCCTGCC	120
TGGTACGCGG	GCCGTGGGAT	CCGGCCCGTG	GGCCGCTTCG	GCCGGCGAAG	AGCTGCCCCG	180
GGGGACGGAC	CCAGGCCTGG	CCCCCGGCGT	GTGCCGGCCT	GCTTCCGCCT	GGAAGGCGGC	240
GCTGAGCCCT	CCCGAGCCCT	CCCCGGGCGG	CTGACGGCCC	AGCTGGTCCA	GGAATAA	297

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...294
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC CTG	48
Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu	
1 5 10 15	
GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG ATC	96
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile	
20 25 30	
CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC GCA GGC CGT GGG ATC CGG	144
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg	
35 40 45	
CCC GTG GGC CGC TTC GGC CGG CGA AGA GCT GCC CTG GGG GAC GGA CCC	192
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly Pro	
50 55 60	
AGG CCT GGC CCC CGG CGT GTG CCG GCC TGC TTC CGC CTG GAA GGC GGT	240
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly	
65 70 75 80	
GCT GAG CCC TCC CGA GCC CTC CCG GGG CGG CTG ACG GCC CAG CTG GTC	288
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val	
85 90 95	
CAG GAA TAA	297
Gln Glu	

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu
1 5 10 15
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile
20 25 30

Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg
		35					40					45			
Pro	Val	Gly	Arg	Phe	Gly	Arg	Arg	Arg	Ala	Ala	Leu	Gly	Asp	Gly	Pro
	50					55					60				
Arg	Pro	Gly	Pro	Arg	Arg	Val	Pro	Ala	Cys	Phe	Arg	Leu	Glu	Gly	Gly
65				70					75					80	
Ala	Glu	Pro	Ser	Arg	Ala	Leu	Pro	Gly	Arg	Leu	Thr	Ala	Gln	Leu	Val
			85					90						95	
Gln	Glu														

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...272
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGCATCATCC AGGAAGACGG AGC ATG GCC CTG AAG ACG TGG CTT CTG TGC TTG	53
Met Ala Leu Lys Thr Trp Leu Leu Cys Leu	
1 5 10	
CTG CTG CTA AGC TTG GTC CTC CCA GGG GCT TCC AGC CGA GCC CAC CAG	101
Leu Leu Leu Ser Leu Val Leu Pro Gly Ala Ser Ser Arg Ala His Gln	
15 20 25	
CAC TCC ATG GAG ACA AGA ACC CCT GAT ATC AAT CCT GCC TGG TAC ACG	149
His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr	
30 35 40	
GGC CGC GGG ATC AGG CCT GTG GGC CGC TTC GGC AGG AGA AGG GCA ACC	197
Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr	
45 50 55	
CCG AGG GAT GTC ACT GGA CTT GGC CAA CTC AGC TGC CTC CCA CTG GAT	245
Pro Arg Asp Val Thr Gly Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp	
60 65 70	
GGA CGC ACC AAG TTC TCT CAG CGT GGA TAACACCCCA GCTCGAGAAG ACAGTGC	299
Gly Arg Thr Lys Phe Ser Gln Arg Gly	
75 80	
TGCTGAGCCC AAGCCCACAC TCCCTGTCCC CTGCAGACCC TCCTCTACCC TCCCTCTCCT	359
CTGCT	364

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met	Ala	Leu	Lys	Thr	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Leu	Ser	Leu	Val
1				5					10					15	
Leu	Pro	Gly	Ala	Ser	Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Thr	Arg
			20					25					30		
Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro
		35					40					45			
Val	Gly	Arg	Phe	Gly	Arg	Arg	Arg	Ala	Thr	Pro	Arg	Asp	Val	Thr	Gly
	50					55					60				
Leu	Gly	Gln	Leu	Ser	Cys	Leu	Pro	Leu	Asp	Gly	Arg	Thr	Lys	Phe	Ser
65					70				75						80
Gln	Arg	Gly													

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...297
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

gtg	ggc	atg	gtg	ggc	aac	gtc	ctg	ctg	gtg	ctg	gtg	atc	gcg	cgg	gtg	48
Val	Gly	Met	Val	Gly	Asn	Val	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val	
1				5					10					15		
cgc	cgg	ctg	cac	aac	gtg	acg	aac	ttc	ctc	atc	ggc	aac	ctg	gcc	ttg	96
Arg	Arg	Leu	His	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	
			20					25					30			
tcc	gac	gtg	ctc	atg	tgc	acc	gcc	tgc	gtg	ccg	ctc	acg	ctg	gcc	tat	144
Ser	Asp	Val	Leu	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	
		35					40					45				
gcc	ttc	gag	cca	cgc	ggc	tgg	gtg	ttc	ggc	ggc	ggc	ctg	tgc	cac	ctg	192
Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	
	50					55					60					
gtc	ttc	ttc	ctg	cag	ccg	gtc	acc	gtc	tat	gtg	tcg	gtg	ttc	acg	ctc	240

Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu
65 70 75 80

acc acc atc gca gtg gac cgg tac gtc gtg ctg gtg cac ccg ctg agg 288
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg
85 90 95

cgg cgc atc 297
Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val
1 5 10 15
Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu
20 25 30
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr
35 40 45
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu
50 55 60
Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu
65 70 75 80
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg
85 90 95
Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...204
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ggc ctg ctg ctg gtc acc tac ctg ctc cct ctg ctg gtc atc ctc ctg 48
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu

1	5	10	15	
tct tac gtc cgg gtg tca gtg aag ctc cgc aac cgc gtg gtg ccg ggc				96
Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly				
	20	25	30	
tgc gtg acc cag agc cag gcc gac tgg gac cgc gct cgg cgc cgg cgc				144
Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg				
	35	40	45	
acc ttc tgc ttg ctg gtg gtg gtc gtg gtg gtg ttt gcc atc tgc tgg				192
Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala Ile Cys Trp				
	50	55	60	
ttg cct tac tac				204
Leu Pro Tyr Tyr				
65				

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu				
1	5	10	15	
Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly				
	20	25	30	
Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg				
	35	40	45	
Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala Ile Cys Trp				
	50	55	60	
Leu Pro Tyr Tyr				
65				

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val	Gly	Met	Val	Gly	Asn	Val	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val
1				5					10					15	
Arg	Arg	Leu	His	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu
			20					25					30		
Ser	Asp	Val	Leu	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr
		35					40					45			
Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu
	50					55					60				
Val	Phe	Phe	Leu	Gln	Pro	Val	Thr	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu
65				70					75					80	
Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg
				85				90					95		
Arg	Arg	Ile	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Tyr	Leu	Leu	Pro	Leu	Leu
			100					105					110		
Val	Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg
		115					120				125				
Val	Val	Pro	Gly	Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala
	130					135					140				
Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe
145					150				155						160
Ala	Ile	Cys	Trp	Leu	Pro	Tyr	Tyr								
				165											

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Leu	Gly	Val	Ser	Gly	Asn	Leu	Ala	Leu	Ile	Ile	Ile	Ile	Leu	Lys	Gln
1				5					10					15	
Lys	Glu	Met	Arg	Asn	Val	Thr	Asn	Ile	Leu	Ile	Val	Asn	Leu	Ser	Phe
			20					25					30		
Ser	Asp	Leu	Leu	Val	Ala	Val	Met	Cys	Leu	Pro	Phe	Thr	Phe	Val	Tyr
		35					40					45			
Thr	Leu	Met	Asp	His	Trp	Val	Phe	Gly	Glu	Thr	Met	Cys	Lys	Leu	Asn
	50					55					60				
Pro	Phe	Val	Gln	Cys	Val	Ser	Ile	Thr	Val	Ser	Ile	Phe	Ser	Leu	Val
65				70					75					80	
Leu	Ile	Ala	Val	Glu	Arg	His	Gln	Leu	Ile	Ile	Asn	Pro	Arg	Gly	Trp
				85					90					95	
Arg	Pro	Asn	Asn	Arg	His	Ala	Tyr	Ile	Gly	Ile	Thr	Val	Ile	Trp	Val
			100					105					110		
Leu	Ala	Val	Ala	Ser	Ser	Leu	Pro	Phe	Val	Ile	Tyr	Gln	Ile	Leu	Thr
		115					120					125			
Asp	Glu	Pro	Phe	Gln	Asn	Val	Ser	Leu	Ala	Ala	Phe	Lys	Asp	Lys	Tyr
	130				135						140				
Val	Cys	Phe	Asp	Lys	Phe	Pro	Ser	Asp	Ser	His	Arg	Leu	Ser	Tyr	Thr
145					150				155						160

Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys Phe Ile Phe
165 170 175
Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg Asn Asn Met
180 185 190
Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu Thr Lys Arg
195 200 205
Ile Asn Val Met Leu Leu Ser Ile Val Val Ala Phe Ala Val Cys Trp
210 215 220
Leu Pro Leu Thr
225

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu
1 5 10 15
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile
20 25 30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
35 40 45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly Pro
50 55 60
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
65 70 75 80
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
85 90 95
Gln Glu

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

gtggaatgaa ggcgggtgggg gacctggctcc tctgacctgct gctgctgggc ctggccctgc 60
agggggctgc cagcagagcc caccagcact ccattggagat ccgcaccccc gacatcaacc 120
ctgcctggta cgcggggccgt gggatccggc ccgtgggccc cttcgccggg cgaagagctg 180
ccccggggga cggaccagg cctggccccc ggcgtgtgcc ggacctgttc cgcctggaag 240
gcggcgctga gccctcccga gccctcccg ggcggctgac ggcccagctg gtccaggaat 300
aacagcggga gcctgcccc caccctcct cctccaccag ccaccttccc tccagtecta 360
ataaaagcag ctggcttgtt 380

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ggcatcatcc aggaagacgg agcatggccc tgaagacgtg gcttctgtgc ttgctgctgc	60
taagcttggt cctcccaggg gcttcaagcc gagcccacca gcactccatg gagacaagaa	120
cccctgatat caatcctgcc tggtagacgg gccgcgggat caggcctgtg ggccgcttcg	180
gcaggagaag ggcaaccccg agggatgtca ctggacttgg ccaactcagc tgcctccac	240
tggatggacg caccaagttc tctcagcgtg gataaacacc cagctcgaga agacagtgtc	300
gctgagccca agcccacact ccctgtcccc tgcagaccct cctctaccct ccctctctc	360
tgct	364

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24..284
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

ggcctcctcg gaggagccaa ggg atg aag gtg ctg agg gcc tgg ctc ctg tgc	53
Met Lys Val Leu Arg Ala Trp Leu Leu Cys	
1 5 10	
ctg ctg atg ctg ggc ctg gcc ctg cgg gga gct gca agt cgt acc cat	101
Leu Leu Met Leu Gly Leu Ala Leu Arg Gly Ala Ala Ser Arg Thr His	
15 20 25	
cgg cac tcc atg gag atc cgc acc cct gac atc aat cct gcc tgg tac	149
Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr	
30 35 40	
gcc agt cgc ggg atc agg cct gtg ggc cgc ttc ggt cgg agg agg gca	197
Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala	
45 50 55	
acc ctg ggg gac gtc ccc aag cct ggc ctg cga ccc cgg ctg acc tgc	245
Thr Leu Gly Asp Val Pro Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys	
60 65 70	

ttc ccc ctg gaa ggc ggt gct atg tcg tcc cag gat ggc tgacagccag 294
Phe Pro Leu Glu Gly Gly Ala Met Ser Ser Gln Asp Gly
75 80 85

cttgtcaaga aactcactct ggagcctccc ccaccccacc ctctcctctc cttcgggctc 354
ctttccc 361

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Lys	Val	Leu	Arg	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Met	Leu	Gly	Leu
1				5					10					15	
Ala	Leu	Arg	Gly	Ala	Ala	Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile
			20					25					30		
Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg
		35					40					45			
Pro	Val	Gly	Arg	Phe	Gly	Arg	Arg	Arg	Ala	Thr	Leu	Gly	Asp	Val	Pro
	50					55					60				
Lys	Pro	Gly	Leu	Arg	Pro	Arg	Leu	Thr	Cys	Phe	Pro	Leu	Glu	Gly	Gly
65				70					75					80	
Ala	Met	Ser	Ser	Gln	Asp	Gly									
				85											

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Lys	Ala	Val	Gly	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Leu	Gly	Leu
1				5					10					15	
Ala	Leu	Gln	Gly	Ala	Ala	Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile
			20					25					30		
Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg
		35					40					45			
Pro	Val	Gly	Arg	Phe	Gly	Arg	Arg	Arg	Ala	Ala	Pro	Gly	Asp	Gly	Pro
	50					55					60				
Arg	Pro	Gly	Pro	Arg	Arg	Val	Pro	Ala	Cys	Arg	Phe	Leu	Glu	Gly	Gly

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1110
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

atg acc tca ctg ccc cct gga acc act ggg gac ccc gat ttg ttt tct	48
Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser	
1 5 10 15	
ggg ccg tcg cca gcc ggc tcc act cca gcc aac cag agt gca gag gct	96
Gly Pro Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala	
20 25 30	
tca gag agc aat gtg tct gcg acg gtt ccc aga gct gca gca gtc acg	144
Ser Glu Ser Asn Val Ser Ala Thr Val Pro Arg Ala Ala Ala Val Thr	
35 40 45	
ccg ttc cag agc ctg caa cta gtg cac cag ctg aag gca ctg atc gtg	192
Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Ala Leu Ile Val	
50 55 60	
atg ctg tac agc atc gtg gtg gtc gtg ggt ctg gtg ggc aac tgc ctt	240
Met Leu Tyr Ser Ile Val Val Val Val Gly Leu Val Gly Asn Cys Leu	
65 70 75 80	
ctt gtg ctg gtg atc gcg cgc gtg cgc cgg ctg cac aac gtg acc aac	288
Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn	
85 90 95	
ttc ctc atc ggc aac ctg gcc ttg tcc gat gtg ctc atg tgt gcc gcc	336
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Ala Ala	
100 105 110	
tgt gtg cct ctc acg ctg gcc tac gcc ttt gaa cct cgt ggc tgg gtg	384
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val	
115 120 125	
ttc ggt gga ggc ctg tgc cac ctt gtt ttc ttc ctg cag ccg gtc acc	432
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr	
130 135 140	
gtc tac gta tcg gtg ttc aca ctc acc aca atc gct gtg gac cgc tat	480
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr	
145 150 155 160	

gtg gtt ctg gtg cac ccg cta cgt cgg cgc att tca ctg aag ctc agc Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Lys Leu Ser 165 170 175	528
gcc tac gct gtg ctg ggc atc tgg gct cta tct gca gtg ctg gcg ctg Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu 180 185 190	576
ccg gcc gcg gtg cac acc tac cat gta gag ctc aag ccc cac gac gtg Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val 195 200 205	624
cgc ctc tgc gag gag ttc tgg ggt tcg cag gag cgc cag cga cag atc Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile 210 215 220	672
tat gcc tgg ggg ctg ctg ctg ggc acc tat ttg ctc ccc ctg ctg gcc Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala 225 230 235 240	720
att ctc ctg tct tac gtc cgg gtg tcg gtg aag ttg cgg aac cgc gtg Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val 245 250 255	768
gtg cct ggc agc gtg acc cag agc cag gct gac tgg gac cga gcg cgt Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg 260 265 270	816
cgc cgt cgc act ttc tgc ctg ctg gtg gtg gtg gtc gtg ttc gcg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala 275 280 285	864
gtc tgc tgg ctg cct ctg cac att ttc aac ctg ctg cgg gac ctg gac Val Cys Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp 290 295 300	912
ccg cgt gcc atc gac ccc tac gcc ttc ggg ctg gtg cag ctc ctc tgc Pro Arg Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys 305 310 315 320	960
cac tgg ctt gcc atg agc tcc gcc tgc tac aac ccc ttc atc tat gcg His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala 325 330 335	1008
tcg ctg cac gac agc ttc cga gag gag cta cgc aag atg ctt ctg tct Ser Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Met Leu Leu Ser 340 345 350	1056
tgg ccc cgc aag atc gtg cct cat ggc cag aat atg acc gtc agt gtg Trp Pro Arg Lys Ile Val Pro His Gly Gln Asn Met Thr Val Ser Val 355 360 365	1104
gtc atc tgatga Val Ile 370	1116

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Thr	Ser	Leu	Pro	Pro	Gly	Thr	Thr	Gly	Asp	Pro	Asp	Leu	Phe	Ser
1				5					10					15	
Gly	Pro	Ser	Pro	Ala	Gly	Ser	Thr	Pro	Ala	Asn	Gln	Ser	Ala	Glu	Ala
			20				25						30		
Ser	Glu	Ser	Asn	Val	Ser	Ala	Thr	Val	Pro	Arg	Ala	Ala	Ala	Val	Thr
			35				40					45			
Pro	Phe	Gln	Ser	Leu	Gln	Leu	Val	His	Gln	Leu	Lys	Ala	Leu	Ile	Val
	50					55					60				
Met	Leu	Tyr	Ser	Ile	Val	Val	Val	Val	Gly	Leu	Val	Gly	Asn	Cys	Leu
65					70					75					80
Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn
				85					90					95	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Ala	Ala
			100					105					110		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
			115				120						125		
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	130					135					140				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
145					150					155					160
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Lys	Leu	Ser
				165					170					175	
Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu
			180					185					190		
Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val
			195				200						205		
Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Ile
	210					215					220				
Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala
225					230					235					240
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
				245					250					255	
Val	Pro	Gly	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
			260					265					270		
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Ala
			275				280						285		
Val	Cys	Trp	Leu	Pro	Leu	His	Ile	Phe	Asn	Leu	Leu	Arg	Asp	Leu	Asp
	290					295					300				
Pro	Arg	Ala	Ile	Asp	Pro	Tyr	Ala	Phe	Gly	Leu	Val	Gln	Leu	Leu	Cys
305					310					315					320
His	Trp	Leu	Ala	Met	Ser	Ser	Ala	Cys	Tyr	Asn	Pro	Phe	Ile	Tyr	Ala
			325						330					335	

[illegible]